1638

RAW SEQUENCE LISTING DATE: 04/08/2002
PATENT APPLICATION: **US/09/534,861A** TIME: 16:09:37

Input Set : **A:\15313SEQ.txt**
Output Set: **N:\CRF3\04082002\I534861A.raw**


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  3 <110> APPLICANT: Smeekens, J.C.M.
  4       Ebskamp, Michael
  5       Geerts, Hendrikis
  6       Weisbeek, Petrus
  8 <120> TITLE OF INVENTION: Production of Oligosaccharides in Transgenic Plants
 10 <130> FILE REFERENCE: ARNO-1-15313
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/534,861A
 13 <141> CURRENT FILING DATE: 2000-03-24
 15 <150> PRIOR APPLICATION NUMBER: US 09/019,385
 16 <151> PRIOR FILING DATE: 1998-02-05
 18 <150> PRIOR APPLICATION NUMBER: US 09/193,385
 19 <151> PRIOR FILING DATE: 1998-11-17
 21 <150> PRIOR APPLICATION NUMBER: US 08/479,470
 22 <151> PRIOR FILING DATE: 1995-06-07
 24 <150> PRIOR APPLICATION NUMBER: NL 1000064
 25 <151> PRIOR FILING DATE: 1995-04-05
 27 <150> PRIOR APPLICATION NUMBER: NL 9401140
 28 <151> PRIOR FILING DATE: 1994-08-07
 30 <160> NUMBER OF SEQ ID NOS: 12
 32 <170> SOFTWARE: PatentIn version 3.0
 34 <210> SEQ ID NO: 1
 35 <211> LENGTH: 2094
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Barley
 39 <220> FEATURE:
 40 <221> NAME/KEY: CDS
 41 <222> LOCATION: (46)..(1923)
 43 <400> SEQUENCE: 1
 44 gctcagaatc taccaaaccc tctcggagtt gacgagcggc gccgc atg ggg tca cac     57
 45                                                    Met Gly Ser His
 46                                                    1
 48 ggc aag cca ccg cta ccg tac gcc tac aag ccg ctg ccc tcg gac gcc      105
 49 Gly Lys Pro Pro Leu Pro Tyr Ala Tyr Lys Pro Leu Pro Ser Asp Ala
 50 5                   10                  15                  20
 52 gcc gac ggt aag cgg acc ggc tgc atg agg tgg tcc gcg tgt gcc acc      153
 53 Ala Asp Gly Lys Arg Thr Gly Cys Met Arg Trp Ser Ala Cys Ala Thr
 54                  25                  30                  35
 56 gtg ctg acg gcc tcg gcc atg gcg gtg gtg gtg gtc ggc gcc acg ctc      201
 57 Val Leu Thr Ala Ser Ala Met Ala Val Val Val Val Gly Ala Thr Leu
 58              40                  45                  50
 60 ctg gcg gga ttg agg atg gag cag gcc gtc gac gag gag gcg gcg gcg      249
 61 Leu Ala Gly Leu Arg Met Glu Gln Ala Val Asp Glu Glu Ala Ala Ala
 62          55                  60                  65
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64 ggc ggg ttc ccg tgg agc aac gag atg ctg cag tgg cag cgc agc ggt      297
65 Gly Gly Phe Pro Trp Ser Asn Glu Met Leu Gln Trp Gln Arg Ser Gly
66      70                  75                  80
68 tac cat ttc cag acg gcc aag aac tac atg agc gat ccc aac ggc ctg      345
69 Tyr His Phe Gln Thr Ala Lys Asn Tyr Met Ser Asp Pro Asn Gly Leu
70  85                  90                  95                 100
72 atg tat tac cgt gga tgg tac cac atg ttc tac cag tac aac ccg gtg      393
73 Met Tyr Tyr Arg Gly Trp Tyr His Met Phe Tyr Gln Tyr Asn Pro Val
74                 105                 110                 115
76 ggc acc gac tgg gac gac ggc atg gag tgg ggc cac gcc gtg tcc cgg      441
77 Gly Thr Asp Trp Asp Asp Gly Met Glu Trp Gly His Ala Val Ser Arg
78             120                 125                 130
80 aac ctt gtc caa tgg cgc acc ctc cct atc gcc atg gtg gcc gac cag      489
81 Asn Leu Val Gln Trp Arg Thr Leu Pro Ile Ala Met Val Ala Asp Gln
82         135                 140                 145
84 tgg tac gac atc ctc gga gtc ctc tcg ggc tcc atg acg gtg cta ccc      537
85 Trp Tyr Asp Ile Leu Gly Val Leu Ser Gly Ser Met Thr Val Leu Pro
86     150                 155                 160
88 aac ggg acg gtc atc atg atc tac acg ggc gcc acc aac gcc tcc gcc      585
89 Asn Gly Thr Val Ile Met Ile Tyr Thr Gly Ala Thr Asn Ala Ser Ala
90 165                 170                 175                 180
92 gtg gag gtc cag tgc atc gcc acc ccg gcc gac ccc aac gac ccc ctc      633
93 Val Glu Val Gln Cys Ile Ala Thr Pro Ala Asp Pro Asn Asp Pro Leu
94                 185                 190                 195
96 ctc cgc cgg tgg acc aag cac ccc gcc aac ccc gtc atc tgg tcg ccg      681
97 Leu Arg Arg Trp Thr Lys His Pro Ala Asn Pro Val Ile Trp Ser Pro
98             200                 205                 210
100 ccg ggg gtc ggc acc aag gat ttc cga gac ccg atg acc gcc tgg tac      729
101 Pro Gly Val Gly Thr Lys Asp Phe Arg Asp Pro Met Thr Ala Trp Tyr
102         215                 220                 225
104 gac gag tcc gac gag aca tgg cgc acc ctc ctc ggg tcc aag gac gac      777
105 Asp Glu Ser Asp Glu Thr Trp Arg Thr Leu Leu Gly Ser Lys Asp Asp
106     230                 235                 240
108 cac gac ggc cac cac gac ggc atc gcc atg atg tac aag acc aag gac      825
109 His Asp Gly His His Asp Gly Ile Ala Met Met Tyr Lys Thr Lys Asp
110 245                 250                 255                 260
112 ttc ctc aac tac gag ctc atc ccg ggc atc ttg cac cgg gtg gtg cgc      873
113 Phe Leu Asn Tyr Glu Leu Ile Pro Gly Ile Leu His Arg Val Val Arg
114                 265                 270                 275
116 acc ggc gag tgg gag tgc atc gac ttc tac ccc gtc ggc cgg aga agc      921
117 Thr Gly Glu Trp Glu Cys Ile Asp Phe Tyr Pro Val Gly Arg Arg Ser
118             280                 285                 290
120 agc gac aac tcg tcg gag atg ctg cac gtg ttg aag gcg agc atg gac      969
121 Ser Asp Asn Ser Ser Glu Met Leu His Val Leu Lys Ala Ser Met Asp
122         295                 300                 305
124 gac gaa cgg cac gac tac tac tcg ctg ggc acg tac gac tcg gcg gcc     1017
125 Asp Glu Arg His Asp Tyr Tyr Ser Leu Gly Thr Tyr Asp Ser Ala Ala
126     310                 315                 320
128 aac acg tgg acg ccc atc gac ccg gag ctc gac ttg ggg atc ggg ctg     1065
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129 Asn Thr Trp Thr Pro Ile Asp Pro Glu Leu Asp Leu Gly Ile Gly Leu
130 325                 330                 335                 340
132 aga tac gac tgg gga aag ttt tat gcg tcc acc tcc ttc tat gat ccg      1113
133 Arg Tyr Asp Trp Gly Lys Phe Tyr Ala Ser Thr Ser Phe Tyr Asp Pro
134                 345                 350                 355
136 gcc aag aac cgg cgc gtg ctc atg ggg tac gtc ggc gag gtc gac tcc      1161
137 Ala Lys Asn Arg Arg Val Leu Met Gly Tyr Val Gly Glu Val Asp Ser
138             360                 365                 370
140 aag cgg gct gat gtc gtc aag gga tgg gct tcc att cag tca gtt cct      1209
141 Lys Arg Ala Asp Val Val Lys Gly Trp Ala Ser Ile Gln Ser Val Pro
142         375                 380                 385
144 agg acg gtg gct ctg gat gag aag acc cgg acg aac ctc ctg ctc tgg      1257
145 Arg Thr Val Ala Leu Asp Glu Lys Thr Arg Thr Asn Leu Leu Leu Trp
146     390                 395                 400
148 ccc gtt gag gag atc gag acc ctc cgc ctc aat gcc acg gaa ctg acc      1305
149 Pro Val Glu Glu Ile Glu Thr Leu Arg Leu Asn Ala Thr Glu Leu Thr
150 405                 410                 415                 420
152 gac gtt acc att aac act ggc tcc gtc atc cat atc ccg ctc cgc caa      1353
153 Asp Val Thr Ile Asn Thr Gly Ser Val Ile His Ile Pro Leu Arg Gln
154                 425                 430                 435
156 ggc act cac gct cga cat gcg gag gcc tct ttc cac ctt gat gct tcc      1401
157 Gly Thr His Ala Arg His Ala Glu Ala Ser Phe His Leu Asp Ala Ser
158             440                 445                 450
160 gcc gtg gct gcc ctc aac gag gcc gat gtg ggc tac aac tgc agt agc      1449
161 Ala Val Ala Ala Leu Asn Glu Ala Asp Val Gly Tyr Asn Cys Ser Ser
162         455                 460                 465
164 agc ggc ggc gct gtt aac cgc ggc gcg cta ggc ccc ttc ggc ctc ctc      1497
165 Ser Gly Gly Ala Val Asn Arg Gly Ala Leu Gly Pro Phe Gly Leu Leu
166     470                 475                 480
168 gtc ctc gcc gcc ggt gac cgc cgt ggc gag caa acg gcg gtc tac ttc      1545
169 Val Leu Ala Ala Gly Asp Arg Arg Gly Glu Gln Thr Ala Val Tyr Phe
170 485                 490                 495                 500
172 tac gtg tct agg ggc ctt gac gga ggc ctc cac acc agc ttc tgc caa      1593
173 Tyr Val Ser Arg Gly Leu Asp Gly Gly Leu His Thr Ser Phe Cys Gln
174                 505                 510                 515
176 gat gag ctg aga tcg tca cga gcc aag gat gtg acc aag cgt gtc atc      1641
177 Asp Glu Leu Arg Ser Ser Arg Ala Lys Asp Val Thr Lys Arg Val Ile
178             520                 525                 530
180 ggg agc acg gtg ccg gtg ctc gac ggt gag gct ttg tca atg agg gtg      1689
181 Gly Ser Thr Val Pro Val Leu Asp Gly Glu Ala Leu Ser Met Arg Val
182         535                 540                 545
184 ctc gtg gat cac tcc atc gtg cag ggc ttc gac atg ggc ggg agg acc      1737
185 Leu Val Asp His Ser Ile Val Gln Gly Phe Asp Met Gly Gly Arg Thr
186     550                 555                 560
188 acg atg acc tcg cgg gtg tac ccg atg gag tcg tat cag gag gca aga      1785
189 Thr Met Thr Ser Arg Val Tyr Pro Met Glu Ser Tyr Gln Glu Ala Arg
190 565                 570                 575                 580
192 gtc tac ttg ttc aac aac gcc acc ggt gcc agc gtg acg gcg gaa agg      1833
193 Val Tyr Leu Phe Asn Asn Ala Thr Gly Ala Ser Val Thr Ala Glu Arg
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194                 585                 590                 595
196 ctg gtc gtg cac gag atg gac tcg gca cac aac cag ctc tcc aat gag     1881
197 Leu Val Val His Glu Met Asp Ser Ala His Asn Gln Leu Ser Asn Glu
198             600                 605                 610
200 gac gat ggc atg tat ctt cat caa gtt ctt gaa tct cgt cat             1923
201 Asp Asp Gly Met Tyr Leu His Gln Val Leu Glu Ser Arg His
202         615                 620                 625
204 taataagcta cattggatca aagaagatca ccagggaagg gcaattcata cataaatcga   1983
206 atcattctgc acaacctcgc ttgcagcatg cattgaaaca tctgtatttg gatcatcttc   2043
208 ttcatttatg tcatagtgaa ctatattact ttgtaaaaaa aaaaaaaaaa a             2094
211 <210> SEQ ID NO: 2
212 <211> LENGTH: 626
213 <212> TYPE: PRT
214 <213> ORGANISM: Barley
216 <400> SEQUENCE: 2
218 Met Gly Ser His Gly Lys Pro Pro Leu Pro Tyr Ala Tyr Lys Pro Leu
219 1               5                   10                  15
222 Pro Ser Asp Ala Ala Asp Gly Lys Arg Thr Gly Cys Met Arg Trp Ser
223             20                  25                  30
226 Ala Cys Ala Thr Val Leu Thr Ala Ser Ala Met Ala Val Val Val Val
227         35                  40                  45
230 Gly Ala Thr Leu Leu Ala Gly Leu Arg Met Glu Gln Ala Val Asp Glu
231     50                  55                  60
234 Glu Ala Ala Ala Gly Gly Phe Pro Trp Ser Asn Glu Met Leu Gln Trp
235 65                  70                  75                  80
238 Gln Arg Ser Gly Tyr His Phe Gln Thr Ala Lys Asn Tyr Met Ser Asp
239                 85                  90                  95
242 Pro Asn Gly Leu Met Tyr Tyr Arg Gly Trp Tyr His Met Phe Tyr Gln
243             100                 105                 110
246 Tyr Asn Pro Val Gly Thr Asp Trp Asp Asp Gly Met Glu Trp Gly His
247         115                 120                 125
250 Ala Val Ser Arg Asn Leu Val Gln Trp Arg Thr Leu Pro Ile Ala Met
251     130                 135                 140
254 Val Ala Asp Gln Trp Tyr Asp Ile Leu Gly Val Leu Ser Gly Ser Met
255 145                 150                 155                 160
258 Thr Val Leu Pro Asn Gly Thr Val Ile Met Ile Tyr Thr Gly Ala Thr
259                 165                 170                 175
262 Asn Ala Ser Ala Val Glu Val Gln Cys Ile Ala Thr Pro Ala Asp Pro
263             180                 185                 190
266 Asn Asp Pro Leu Leu Arg Arg Trp Thr Lys His Pro Ala Asn Pro Val
267         195                 200                 205
270 Ile Trp Ser Pro Pro Gly Val Gly Thr Lys Asp Phe Arg Asp Pro Met
271     210                 215                 220
274 Thr Ala Trp Tyr Asp Glu Ser Asp Glu Thr Trp Arg Thr Leu Leu Gly
275 225                 230                 235                 240
278 Ser Lys Asp Asp His Asp Gly His His Asp Gly Ile Ala Met Met Tyr
279                 245                 250                 255
282 Lys Thr Lys Asp Phe Leu Asn Tyr Glu Leu Ile Pro Gly Ile Leu His
283             260                 265                 270
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286 Arg Val Val Arg Thr Gly Glu Trp Glu Cys Ile Asp Phe Tyr Pro Val
287         275                 280                 285
288 Gly Arg Arg Ser Ser Asp Asn Ser Ser Glu Met Leu His Val Leu Lys
289     290                 295                 300
290 Ala Ser Met Asp Asp Glu Arg His Asp Tyr Tyr Ser Leu Gly Thr Tyr
291 305                 310                 315                 320
292 Asp Ser Ala Ala Asn Thr Trp Thr Pro Ile Asp Pro Glu Leu Asp Leu
293                 325                 330                 335
294 Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Phe Tyr Ala Ser Thr Ser
295             340                 345                 350
296 Phe Tyr Asp Pro Ala Lys Asn Arg Arg Val Leu Met Gly Tyr Val Gly
297         355                 360                 365
298 Glu Val Asp Ser Lys Arg Ala Asp Val Val Lys Gly Trp Ala Ser Ile
299     370                 375                 380
300 Gln Ser Val Pro Arg Thr Val Ala Leu Asp Glu Lys Thr Arg Thr Asn
301 385                 390                 395                 400
302 Leu Leu Leu Trp Pro Val Glu Glu Ile Glu Thr Leu Arg Leu Asn Ala
303                 405                 410                 415
304 Thr Glu Leu Thr Asp Val Thr Ile Asn Thr Gly Ser Val Ile His Ile
305             420                 425                 430
306 Pro Leu Arg Gln Gly Thr His Ala Arg His Ala Glu Ala Ser Phe His
307         435                 440                 445
308 Leu Asp Ala Ser Ala Val Ala Ala Leu Asn Glu Ala Asp Val Gly Tyr
309     450                 455                 460
310 Asn Cys Ser Ser Ser Gly Gly Ala Val Asn Arg Gly Ala Leu Gly Pro
311 465                 470                 475                 480
312 Phe Gly Leu Leu Val Leu Ala Ala Gly Asp Arg Arg Gly Glu Gln Thr
313                 485                 490                 495
314 Ala Val Tyr Phe Tyr Val Ser Arg Gly Leu Asp Gly Gly Leu His Thr
315             500                 505                 510
316 Ser Phe Cys Gln Asp Glu Leu Arg Ser Ser Arg Ala Lys Asp Val Thr
317         515                 520                 525
318 Lys Arg Val Ile Gly Ser Thr Val Pro Val Leu Asp Gly Glu Ala Leu
319     530                 535                 540
320 Ser Met Arg Val Leu Val Asp His Ser Ile Val Gln Gly Phe Asp Met
321 545                 550                 555                 560
322 Gly Gly Arg Thr Thr Met Thr Ser Arg Val Tyr Pro Met Glu Ser Tyr
323                 565                 570                 575
324 Gln Glu Ala Arg Val Tyr Leu Phe Asn Asn Ala Thr Gly Ala Ser Val
325             580                 585                 590
326 Thr Ala Glu Arg Leu Val Val His Glu Met Asp Ser Ala His Asn Gln
327         595                 600                 605
328 Leu Ser Asn Glu Asp Asp Gly Met Tyr Leu His Gln Val Leu Glu Ser
329     610                 615                 620
330 Arg His
331 625
332 <210> SEQ ID NO: 3
333 <211> LENGTH: 30
334 <212> TYPE: DNA
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FYI

VERIFICATION SUMMARY DATE: 04/08/2002
PATENT APPLICATION: **US/09/534,861A** TIME: 16:09:38

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Output Set: **N:\CRF3\04082002\I534861A.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:474 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12